IN THE SPECIFICATION:

At page 1, after line 2 substitute the following paragraph:

This application is a ~~divisen~~ divisional of U.S. Serial No. 09/059,461, filed April 14, 1998, ~~allowed~~ now U.S. Patent No. 6,146,894.

At page 19, line 14 to page 20, line 8, substitute the following paragraph:

In vitro translation. Linear DNA fragments containing *hPMS2* and *hMLH1* cDNA sequences were prepared by PCR, incorporating sequences for *in vitro* transcription and translation in the sense primer. A full-length *hMLH1* fragment was prepared using the sense primer 5'-ggatcctaatacgactcactatagggaga ccaccatgtcgttcgtggcaggg-3' (codons 1-6; SEQ ID NO: 3) and the antisense primer 5'-taagtcttaagtgctaccaac-3' (SEQ ID NO: 4; located in the 3' untranslated region, nt 2411-2433), using a wild-type *hMLH1* cDNA clone as template. A full-length *hPMS2* fragment was prepared with the sense primer comprising ~~5'-ggatcctaatacgactcactatagggagaccaccatggaacaattgcctgcgg-3'~~ 5'- atg gag cga gct gag agc-3' (codons 1- 6; SEQ ID NO: 5) and the antisense primer 5'-aggttagtgaagactctgtc-3' (SEQ ID NO: 6; located in 3' untranslated region, nt 2670-2690) using a cloned *hPMS2* cDNA as template. A fragment encoding the amino-terminal 134 amino acids of hPMS2 was prepared using the same sense primer and the antisense primer 5'-agtcgagttccaaccttcg-3 (SEQ ID NO: 7). A fragment containing codons 135 - 862 of *hPMS135* was generated using the sense primer 5'-ggatcctaatacgactcactatagggagaccaccatgatgtttgatcacaatgg-3' (SEQ ID NO: 8; codons 135-141) and the same antisense primer as that used for the full-length *hPMS2* protein. These fragments were used to produce proteins via the coupled transcription-translation system (Promega). The reactions were supplemented with ^{35}S-labelled methionine or unlabelled methionine, as indicated in the text. The PMS135 and hMLH1 proteins could not be simultaneously radiolabelled and immunoprecipitated because of their similar molecular weights precluded resolution. Lower molecular weight bands are presumed to be degradation products and/or polypeptides translated from alternative internal methionines.

After the claims add the enclosed sequence listing to the application.